

J. MURPHY

1644 RUSH

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/313,299B

DATE: 03/29/2000
TIME: 10:10:42

Input Set: I313299B.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

P.5

ENTERED

1 <110> APPLICANT: Lee, James
2 Wood, William I.
3 <120> TITLE OF INVENTION: VEGF-RELATED PROTEIN
4 <130> FILE REFERENCE: P0963R1D1
5 <140> CURRENT APPLICATION NUMBER: US/09/313,299B
6 <141> CURRENT FILING DATE: 1999-05-17
7 <150> EARLIER APPLICATION NUMBER: US 08/706,054
8 <151> EARLIER FILING DATE: 1996-08-30
9 <150> EARLIER APPLICATION NUMBER: US 60/003,491
10 <151> EARLIER FILING DATE: 1995-09-08
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18 <222> LOCATION: 1-2031
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23 ccgaatgcgg ggagctcgga tgtccggttt cctgtgaggc ttttacctga 150
24 caccgcggc ctttccccgg cactggctgg gagggcgccc tgcaaagtgt 200
25 ggaacgcgga gccccggacc cgctcccgcc gcctccgggt cgcccagggg 250
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27 tcgcagggggc gcccgcgccc ccaccctgc ccccgccagc ggaccggtcc 350
28 cccacccccg gtccttcac catgcacttg ctgggcttct tctctgtggc 400
29 gtgttctctg ctgcgcgctg cgctgctccc gggtcctcgc gaggcgcccg 450
30 ccgccgcccgc cgccttcgag tccggactcg acctctcgga cgcggagccc 500
31 gacgcgggcg aggccacggc ttatgcaagc aaagatctgg aggagcagtt 550
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33 attggaatat gtacaagtgt cagctaagga aaggaggctg gcaacataac 650
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35 tgcagcacat tataatacag agatcttgaa aagtattgat aatgagtggg 750
36 gaaagactca atgcatgcc cgggaggtgt gtatagatgt ggggaaggag 800
37 tttggagtcg cgacaaacac cttctttaa cctccatgtg tgtccgtcta 850
38 cagatgtggg ggttgctgca atagtgggg gctgcagtgc atgaacacca 900
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40 caaggcccca aaccagtaac aatcagtttt gccaatcaca ctccctgccg 1000
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43 cccaccaatt acatgtggaa taatcacatc tgcagatgcc tggctcagga 1150
44 agattttatg ttttcctcgg atgctggaga tgactcaaca gatggattcc 1200

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47      agacagaaac tcatgccagt gtgtctgtaa aaacaaactc tccccagcc 1350
48      aatgtggggc caaccgagaa tttgatgaaa acacatgcca gtgtgtatgt 1400
49      aaaagaacct gccccagaaa tcaaccctta aatcctggaa aatgtgcctg 1450
50      tgaatgtaca gaaagtccac agaaatgctt gttaaaagga aagaagttcc 1500
51      accaccaaac atgcagctgt tacagacggc catgtacgaa ccgccagaag 1550
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53      ttcataattgg aaaagaccac aaatgagcta agattgtact gttttccagt 1650
54      tcatcgattt tctattatgg aaaactgtgt tgccacagta gaactgtctg 1700
55      tgaacagaga gacccttgtg ggtccatgct aacaaagaca aaagtctgtc 1750
56      tttcctgaac catgtggata actttacaga aatggactgg agctcatctg 1800
57      caaaaggcct cttgtaaaga ctggttttct gccaatgacc aaacagccaa 1850
58      gattttcctc ttgtgatttc tttaaaagaa tgactatata atttatttcc 1900
59      actaaaaata ttgtttctgc attcattttt atagcaacaa caattggtaa 1950
60      aactcactgt gatcaatatt tttatatcat gcaaaatatg tttaaaataa 2000
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67      <221> NAME/KEY: Human
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72      catgatataa aaatattgat cacagtgagt tttaccaatt gttgttgcta 100
73      taaaaatgaa tgcagaaaca atatttttag tggaaataaa ttatatagtc 150
74      attcttttaa agaaatcaca agaggaaaat cttggctggt tggtcattgg 200
75      cagaaaacca gtctttacaa gaggcctttt gcagatgagc tccagtccat 250
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80      cttcactata tgaaaatcct ggctcacaa gcttctggcg gttcgtacat 500
81      ggccgtctgt aacagctgca tgtttggtgg tggaaacttct ttccttttaa 550
82      caagcatttc tgtggacttt ctgtacattc acaggcacat tttccaggat 600
83      ttagggggtg atttctgggg caggttcctt tacatacaca ctggcatgtg 650
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90      tgacactgtg gtagtggtgc tggcagggaa cgtctaataa tggaatgaac 1000
91      ttgtctgtaa acatccagtt tagacatgca tcggcaggaa gtgtgattgg 1050
92      caaaactgat tgttactggg ttggggcctt gagagagagg cactgtaatt 1100
93      tcaataacg tcttgctgag gtagctctgt ctggtgttca tgcactgcag 1150
94      ccctcacta ttgcagcaac cccacatct gtagacggac acacatggag 1200

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95      gtttaaagaa ggtgtttgtc gcgactccaa actccttccc cacatctata 1250
96      cacacctccc gtggcatgca ttgagtcttt ctccactcat tatcaatact 1300
97      tttcaagatc tctgtattat aatgtgctgc agcaaatttt atagtctctt 1350
98      ctgtccttga gttgaggttg gcctgttctc tgttatgttg ccagcctcct 1400
99      ttccttagct gacacttgta ctttttccaa tattctgggt agagtacagt 1450
100     catgagttca tctacactgg acacagaccg taactgctcc tccagatctt 1500
101     tgcttgcata agccgtggcc tcgcccgcgt cgggctccgc gtccgagagg 1550
102     tcgagtcagg actcgaaggc ggcggcgggc gcgggcgctt cgcgaggacc 1600
103     cgggagcagc acagcggcga gcagagaaca cgccacagag aagaagccca 1650
104     gcaagtgcac ggtggaagga ccgggggttg gggaccggtc cgctggcggg 1700
105     ggcaggggtg ggggcgcggg cggccctgcg aggcgcggg cccctcctgg 1750
106     tccctctccc ccgggctcct cccggcgacc cccctgggc gagccggagg 1800
107     cggcgggagc gggtcggggg ctccgcgttc ccaactttgc agggcgccct 1850
108     cccagccagt accggggaaa ggcggcgggg gtcaggtaaa agcctcacag 1900
109     gaaaccggac atccgagctc cccgcattcg gagccgcga ggtgaagcga 1950
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<210> SEQ ID NO 3

<211> LENGTH: 419

<212> TYPE: PRT

<213> ORGANISM: Human

<220> FEATURE:

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<222> LOCATION: 1-419

<223> OTHER INFORMATION: Sequence source: VRP

<400> SEQUENCE: 3

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122           1           5           10           15
123     Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala
124           20           25           30
125     Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
126           35           40           45
127     Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu
128           50           55           60
129     Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
130           65           70           75
131     Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
132           80           85           90
133     Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu
134           95          100          105
135     Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
136          110          115          120
137     Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
138          125          130          135
139     Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr
140          140          145          150
141     Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
142          155          160          165
143     Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr
144          170          175          180

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145	Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly		
146		185	190
147	Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg		
148		200	205
149	Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile		
150		215	220
151	Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn		
152		230	235
153	Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg		
154		245	250
155	Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp		
156		260	265
157	Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu		
158		275	280
159	Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg		
160		290	295
161	Pro Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys		
162		305	310
163	Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala		
164		320	325
165	Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg		
166		335	340
167	Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys		
168		350	355
169	Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys		
170		365	370
171	Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr Asn		
172		380	385
173	Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val		
174		395	400
175	Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met Ser		
176		410	415
177	<210> SEQ ID NO 4		419
178	<211> LENGTH: 147		
179	<212> TYPE: PRT		
180	<213> ORGANISM: Human		
181	<220> FEATURE:		
182	<221> NAME/KEY: Human		
183	<222> LOCATION: 1-147		
184	<223> OTHER INFORMATION: Sequence source: VEGE-121		
185	<400> SEQUENCE: 4		
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187	1	5	10
188	Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala		
189		20	25
190	Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp		
191		35	40
192	Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp		
193		50	55
194	Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro		

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195          65          70          75
196      Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
197          80          85          90
198      Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln
199          95         100         105
200      Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met
201         110         115         120
202      Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp
203         125         130         135
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205         140         145         147
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207      <211> LENGTH: 149
208      <212> TYPE: PRT
209      <213> ORGANISM: Human
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211      <221> NAME/KEY: Human
212      <222> LOCATION: 1-149
213      <223> OTHER INFORMATION: Sequence source: PIGE-131
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216          1          5          10          15
217      Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser
218          20          25          30
219      Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu
220          35          40          45
221      Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp
222          50          55          60
223      Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro
224          65          70          75
225      Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu
226          80          85          90
227      Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln
228          95         100         105
229      Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu
230         110         115         120
231      Thr Phe Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu
232         125         130         135
233      Lys Met Lys Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg
234         140         145         149
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236      <211> LENGTH: 299
237      <212> TYPE: DNA
238      <213> ORGANISM: Unknown
239      <220> FEATURE:
240      <223> OTHER INFORMATION: Sequence source: EST
241      <220> FEATURE:
242      <221> NAME/KEY: unsure
243      <222> LOCATION: 74
244      <223> OTHER INFORMATION: unknown base

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/313,299B

DATE: 03/29/2000
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Line ? Error/Warning

Original Text

247 W "N" or "Xaa" used: Feature required

aacaccagca cgagctacct cagnaagacg ttatttga